

```

EDA 1 MGYPEVERRELLPAAAPRERGSQGCCGAPARAGEGNSCLFLGFFGLSLALHLLTLCQ
TA MGYPEVERREPLPAAAPRERGSQGCCGCRGAPARAGEGNSCRFLGFFGLSLALHLLTLCQ
*****
61 YLELRSELRRERGAESRLGSGTPTGTSGLSLGGLDPDSPITSHLGQSPKQPLEPGE
TA YLELRSELRRERGTERLGGPGAPGTSGTLSSPGSLDPVGPITRHLGQPSFQQPLEPGE
*****
121 AALHSDSQDGHQQMALLNFFFPDEKPYSEESRRVRNRKRSKNEGADGPVKNKKKGKKAG
TA DPLPPESQDRHQQMALLNFFFPDEKAYSEESRRVRNRKRSKSEGADGPVKNKKKGKKAG
*****
181 PPGPNGPPPPGPPGPPGIPGIPGTTVMGPPGPPGPPGPPGLQGPSGAADK
TA PPGPNGPPPPGPPGPPGIPGIPGTTVMGPPGPPGPPGPPGLQGPSGAADK
*****
241 AGTRENQPAVVHLQGGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGEVLVDGT
TA TGTRENQPAVVHLQGGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGEVLVDGT
*****
301 YFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
TA YFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
*****
361 AVKMOVHADISINMSKHTTFFGAIRLGEAPAS
TA AVKMOVHADISINMSKHTTFFGAIRLGEAPAS
*****

```

FIG. 1

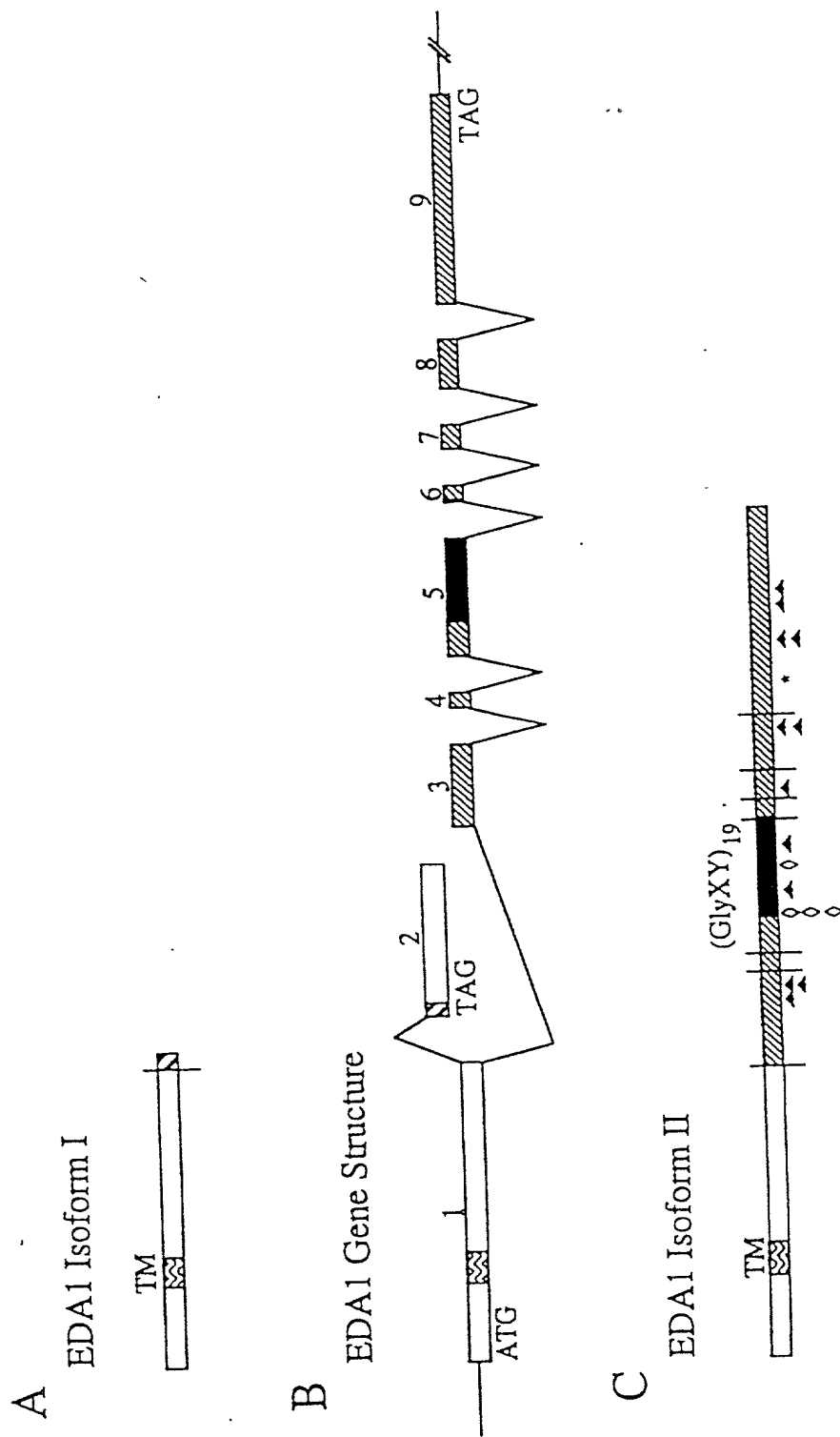


FIG. 2



FIG. 3

EDA	L	E	V	L	V	D	G	T	Y	F	I	Y	S	Q	V	E	V
HuTNF	L	V	V	P	S	E	G	L	Y	L	I	Y	S	Q	V	L	F
CD40L	L	T	V	K	R	Q	G	L	Y	Y	I	Y	A	Q	V	T	F
LT $\alpha$	L	L	V	P	T	S	G	I	Y	F	V	Y	S	Q	V	V	F
LT $\beta$	L	A	L	P	Q	D	G	L	Y	Y	L	Y	C	L	V	G	Y
FAS	L	V	I	N	E	A	G	L	Y	F	V	Y	S	K	V	Y	F
CD40L	L	T	V	K	R	Q	G	L	Y	Y	I	Y	A	Q	V	T	F

FIG. 4

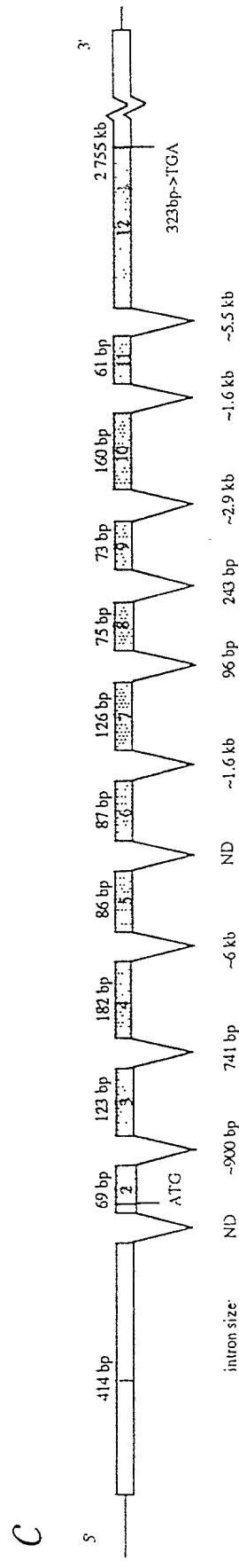
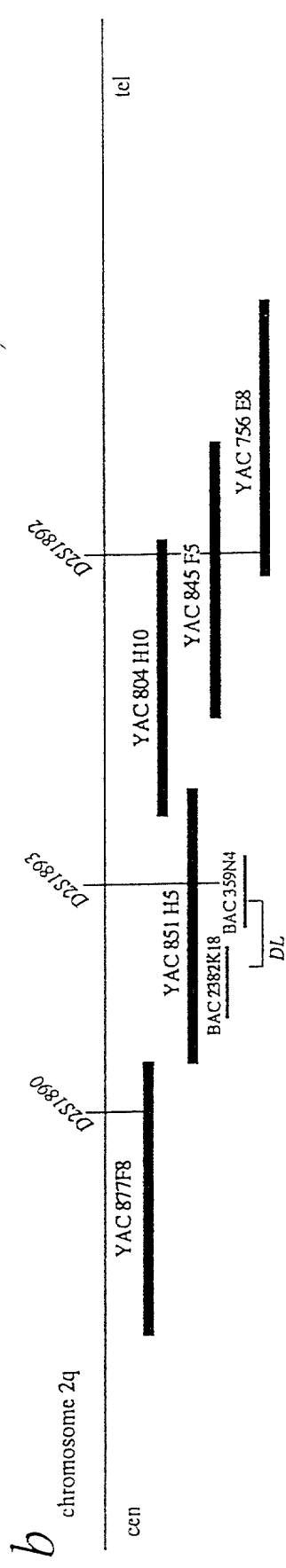
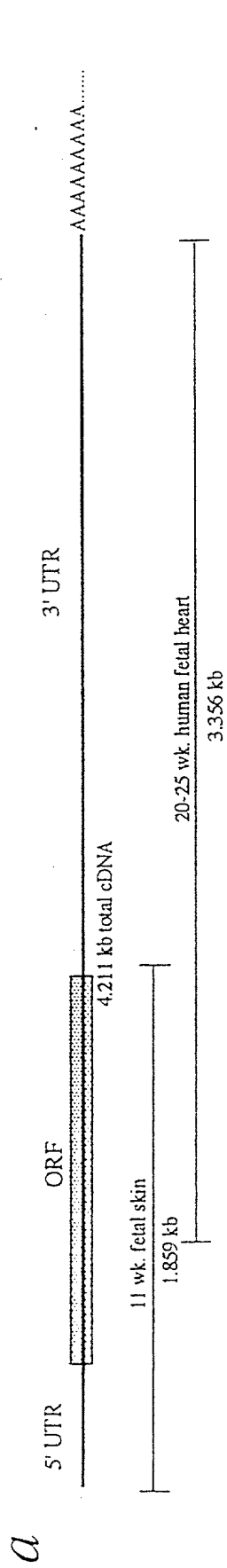


FIG. 5

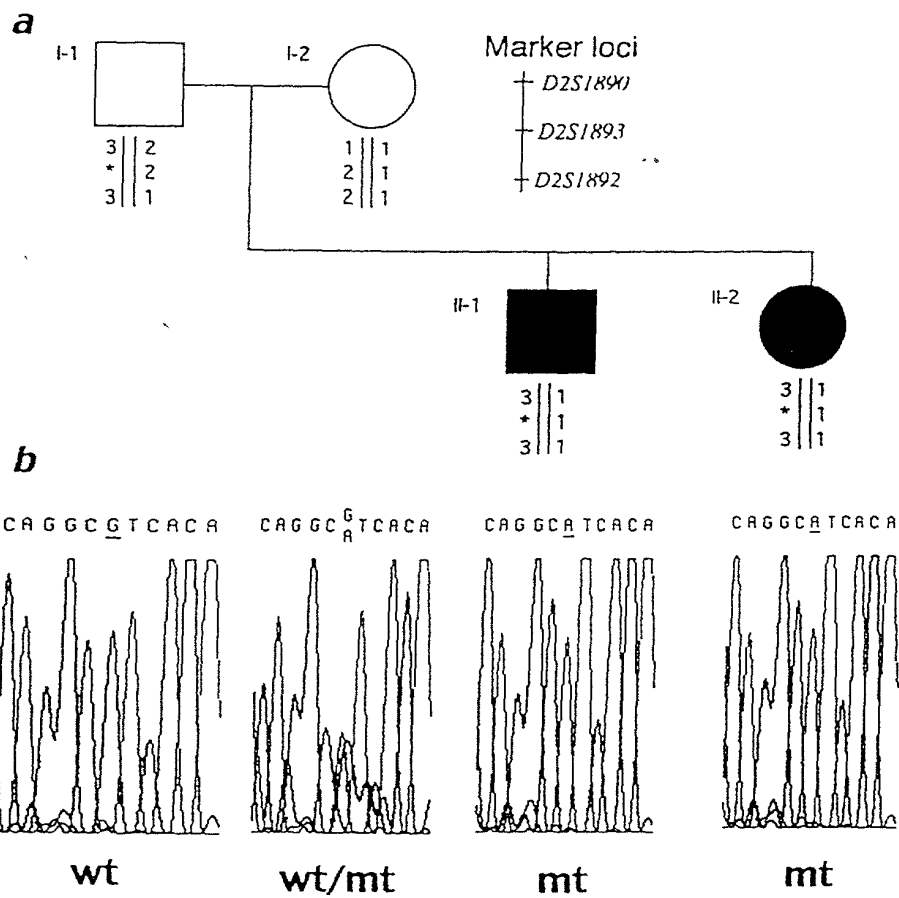


FIG. 6

DL	1	MAHVGDC	TQT	PWLPVLVVSL	MCSARAEYSN	CGENEYYNQT	TGLCQECPPC
dL	1	MAHVGDC	KWM	SWLPVLVVSL	MCSAKAEDSN	CGENEYHNQT	TGLCQQCPPC
DL	51	GPGE	E	PYLSC	GYGTKDEDYG	CVP	CPAEKFS
dL	51	RPGE	E	PYMSC	GYGTKDDDYG	CVP	CPAEKFS
DL	101	VLTPGDMEND	AECGPCLPGY	YMLENRPRNI	YGMVCYSCLL	APPNTKECVG	
dL	101	VLTPGDMEND	AECGPCLPGY	YMLENRPRNI	YGMVCYSCLL	APPNTKECVG	
DL	151	ATSGASANFP	GTSGSSTLSP	FQHAHKELSG	QGH	LATALII	AMSTIFIMAI
dL	151	ATSGVSAHSS	STSGGSTLSP	FQHAHKELSG	QGH	LATALII	AMSTIFIMAI
DL	201	AIVLIIMFYI	LKTKPSAPAC	CTSHPGKSVE	AQVSKDEEKK	EAPDNVVMFS	
dL	201	AIVLIIMFYI	MKTKPSAPAC	CSSPPGKSAE	APANTHEEKK	EAPDSVVTFP	
DL	251	EKDEF	EKLTA	TSAKPTKSEN	DASSENEQLL	SRSVDSDEEP	APDKQGSPEL
dL	251	ENG	FQKLTA	TPTKTPKSEN	DASSENEQLL	SRSVDSDEEP	APDKQGSPEL
DL	301	CLLSLVHLAR	EKSATSNKSA	GIQSRRRKIL	DVYANVCGVV	EGLSPTELPF	
dL	301	CLLSLVHLAR	EKSVTSNKSA	GIQSRRRKIL	DVYANVCGVV	EGLSPTELPF	
DL	351	DCLEKTSRML	SSTYNSEKAV	VKTWRHLAES	FGLKRDEIGG	MTDGMQLFDR	
dL	351	DCLEKTSRML	SSTYNSEKAV	VKTWRHLAES	FGLKRDEIGG	MTDGMQLFDR	
DL	401	ISTAGYSIPE	LLTKLVQIER	LDAVESLCAD	I	LEWAGVVPP	ASQPHAAS
dL	401	ISTAGYSIPE	LLTKLVQIER	LDAVESLCAD	I	LEWAGVVPP	ASPPPAAS

FIG. 7

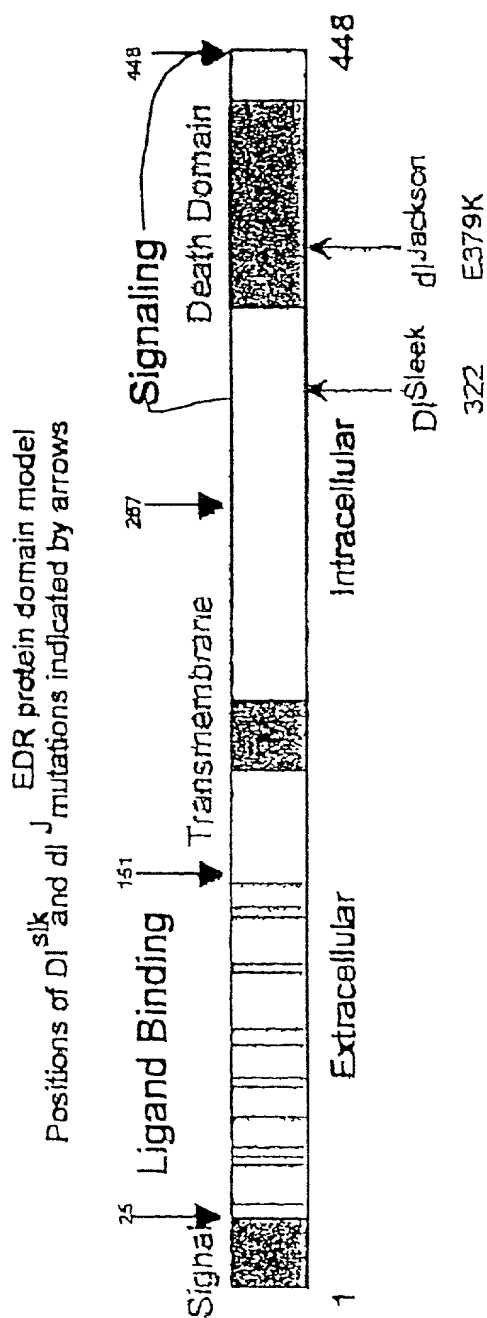


FIG. 8